

Fig. 1

22

a

2

a

a

a

-3-

BstAPI | TatI |
 721 GCCGGGGCAGTCGTTGCTATGCCCCCTTGCAGGAGTATTGGTGCAGTACATTGGCTGGGCC 780
 -----+-----+-----+-----+-----+
 CGGCCCCGTCAGCAACGATACGGGGAACGTCCTCATAACCACGTCATGTAACCGACCCGG
 a A G A V V A M P L A G V L V Q Y I G W A -

 BsgI | PciI |
 781 TCTGCCTTTTATATTTACGGGATGTTTGGGAATTATTTGGTACATGTTTTGGCTGCTGCTG 840
 -----+-----+-----+-----+-----+
 AGACGGAAATATAAATGCCCTACAAACCTTAATAAACCATGTACAAAACCGACGACGAC
 a S A F Y I Y G M F G I I W Y M F W L L L -

 PstI | HphI |
 841 CAGGCTTATGAGTGTCCAGCAGTTCACCCAACAATATCCAATGAAGAACGGACCTACATA 900
 -----+-----+-----+-----+-----+
 GTCCGAATACTCACAGGTCGTCAAGTGGGTTGTTATAGGTTACTTCTTGCCTGGATGTAT
 a Q A Y E C P A V H P T I S N E E R T Y I -

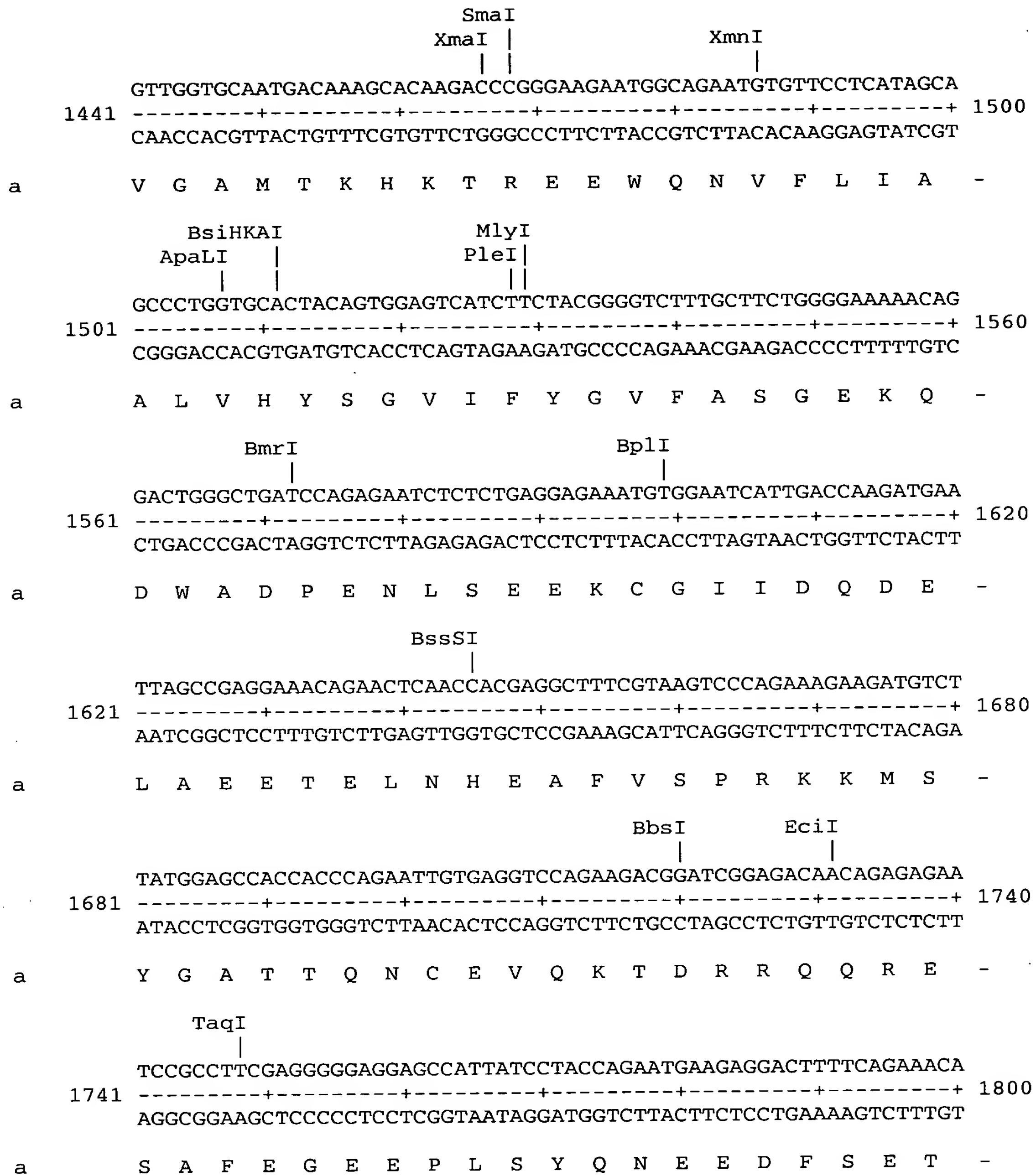
 BbeI
 HaeII
 HhaI |
 SfoI ||
 BsaHI ||
 HinPII ||
 NarI ||
 KasI ||| BglI | MscI
 NcoI |
 901 GAGACAAGTATAGGAGAAGGCGCCAACCTTGGCCAGTCTGAGCAAATTCAACACACCATGG 960
 -----+-----+-----+-----+-----+
 CTCTGTTCATATCCTCTTCCGCGGTTGAACCGGTCAGACTCGTTTAAGTTGTGTGGTACC
 a E T S I G E G A N L A S L S K F N T P W -

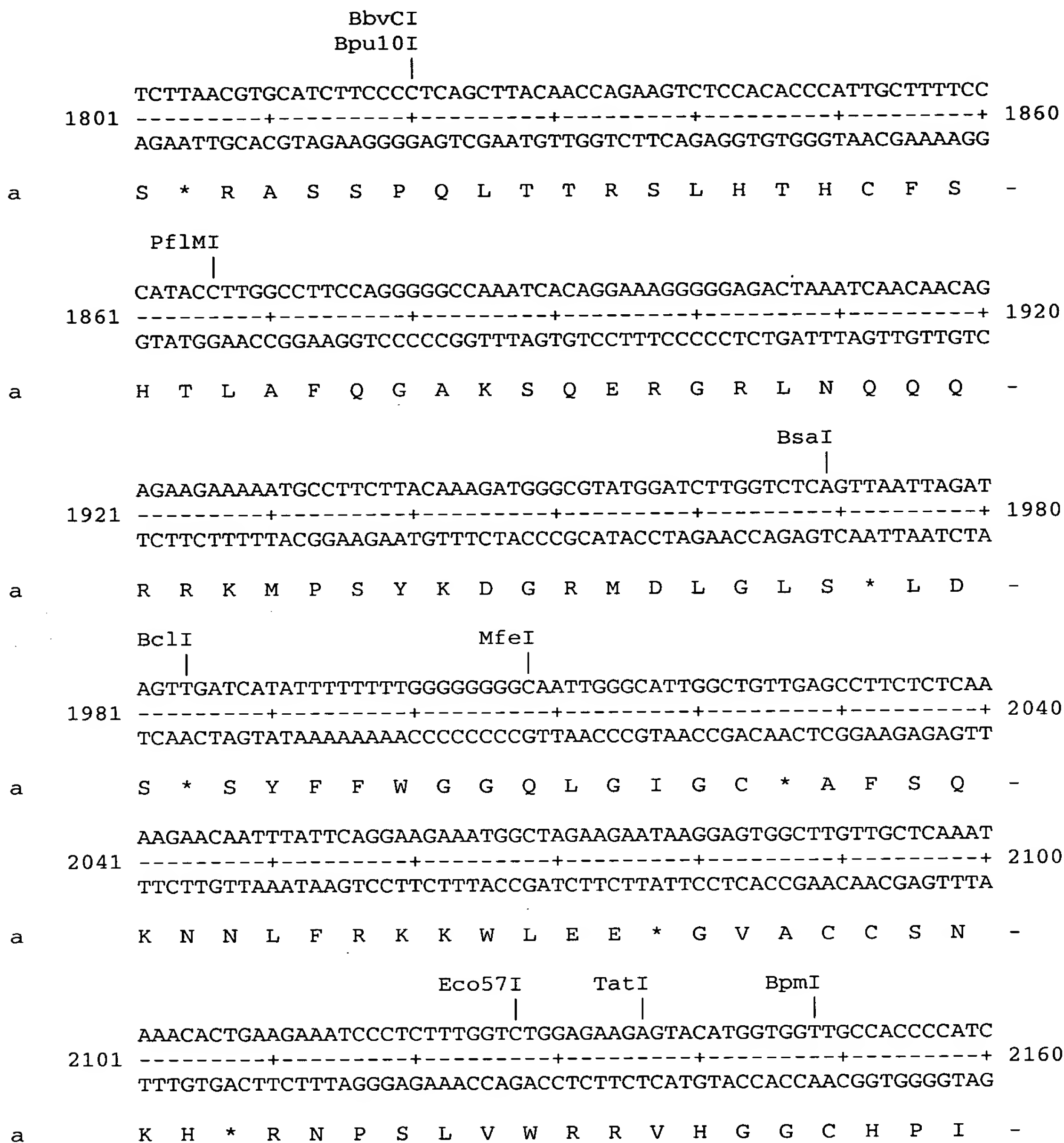
 BstXI |
 961 AGAAGGTTTTTCACATCCTTGCCTGTCTATGCCATTATTGTGGCAAACTTTTGTAGAAGC 1020
 -----+-----+-----+-----+-----+
 TCTTCCAAAAAGTGTAGGAACGGACAGATACGGTAATAACACCGTTTGAAAACATCTTCG
 a R R F F T S L P V Y A I I V A N F C R S -

Fig. 1 cont'd

TGGACCTTCTATTTGCTCTTAATAAGTCAGCCTGCTTACTTTGAAGAGGTCTTTGGGTTT
 1021 -----+-----+-----+-----+-----+-----+ 1080
 ACCTGGAAGATAAACGAGAATTATTCAGTCGGACGAATGAAACTTCTCCAGAAACCCAAA
 a W T F Y L L L I S Q P A Y F E E V F G F -
 BsaI PvuII DraIII BsaBI HphI Acc65I
 | | | | |
 GCAATAAGTAAGGTGGGTCTCTTGTCAGCTGTCCACACATGGTGATGACAATCGTGGTA
 1081 -----+-----+-----+-----+-----+-----+ 1140
 CGTTATTCATTCCACCCAGAGAACAGTCGACAGGGTGTGTACCACTACTGTTAGCACCAT
 a A I S K V G L L S A V P H M V M T I V V -
 KpnI
 |
 CCCATTGGAGGACAACTGGCTGATTATTTAAGAAGCCGAAAGATTTTGACCACAACTGCT
 1141 -----+-----+-----+-----+-----+-----+ 1200
 GGGTAACCTCCTGTTGACCGACTAATAAATTCTTCGGCTTTCTAAAACTGGTGTGACGA
 a P I G G Q L A D Y L R S R K I L T T T A -
 BspHI
 |
 GTCAGAAAGATCATGAATTGTGGAGGCTTTGGCATGGAGGCAACCTTGCTCCTGGTGGTT
 1201 -----+-----+-----+-----+-----+-----+ 1260
 CAGTCTTTCTAGTACTTAACACCTCCGAAACCGTACCTCCGTTGGAACGAGGACCACCAA
 a V R K I M N C G G F G M E A T L L L V V -
 BstXI
 |
 GGGTTTTCCCATACCAAAGGAGTGGCTATCTCCTTCCTGGTGCTTGCTGTAGGATTTAGT
 1261 -----+-----+-----+-----+-----+-----+ 1320
 CCCAAAAGGGTATGGTTTCCTCACCGATAGAGGAAGGACCACGAACGACATCCTAAATCA
 a G F S H T K G V A I S F L V L A V G F S -
 GGCTTTGCAATTTTCAGGTTTCAATGTCAACCACCTGGACATTGCTCCACGATATGCCAGC
 1321 -----+-----+-----+-----+-----+-----+ 1380
 CCGAAACGTAAAGTCAAAGTTACAGTTGGTGGACCTGTAACGAGGTGCTATACGGTCG
 a G F A I S G F N V N H L D I A P R Y A S -
 XcmI
 |
 ATCCTCATGGGGATCTCAAATGGCGTGGGAACCCTCTCTGGAATGGTTTGTCCCCTCATT
 1381 -----+-----+-----+-----+-----+-----+ 1440
 TAGGAGTACCCCTAGAGTTTACCGCACCCCTTGGGAGAGACCTTACCAAACAGGGGAGTAA
 a I L M G I S N G V G T L S G M V C P L I -

Fig. 1 cont'd

**Fig. 1 cont'd**

**Fig. 1 cont'd**

[illegible]

Fig. 1 cont'd

2581

Fig. 1 cont'd

09515101 070404
40420 197560

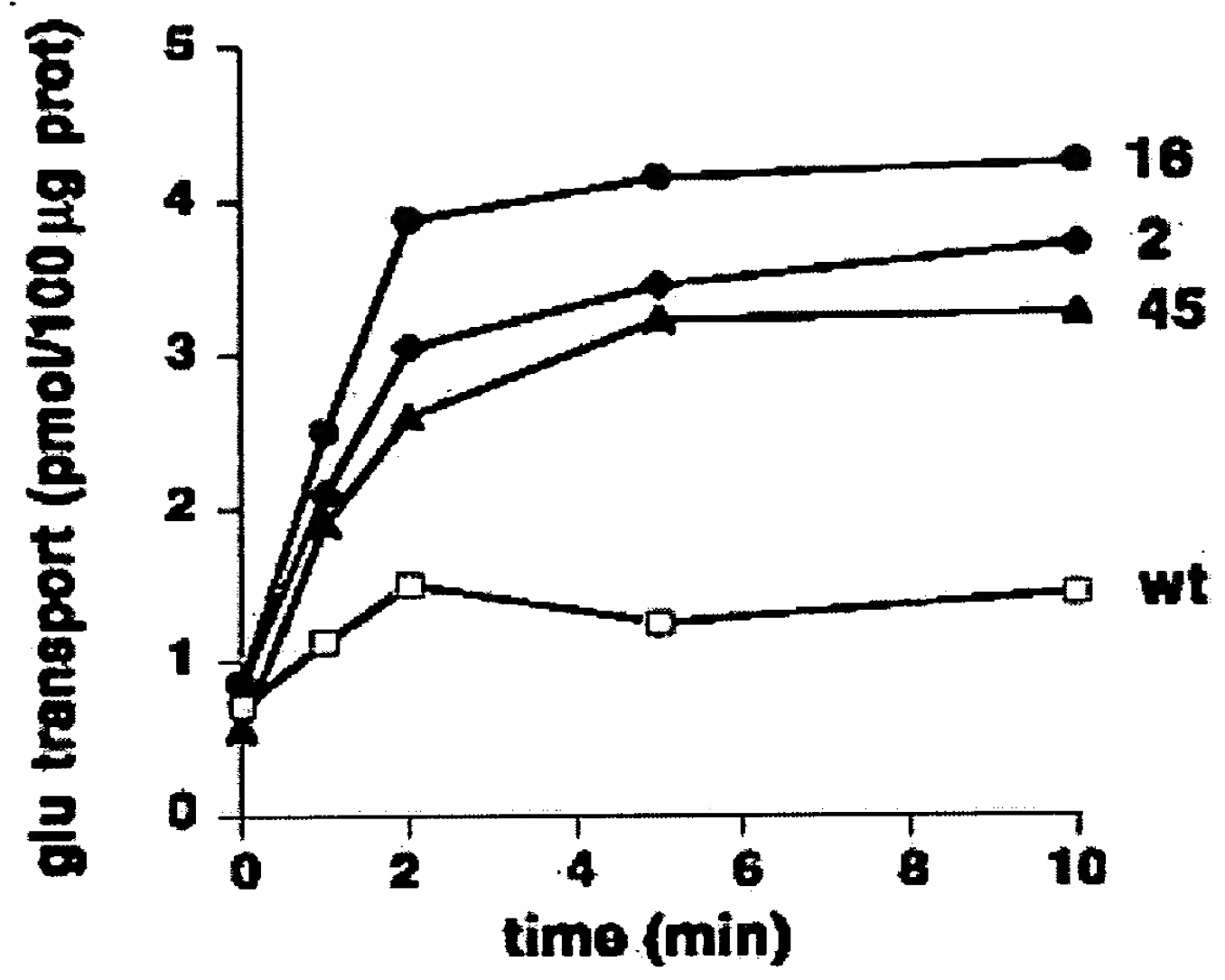


Fig. 2A

094220-1310350

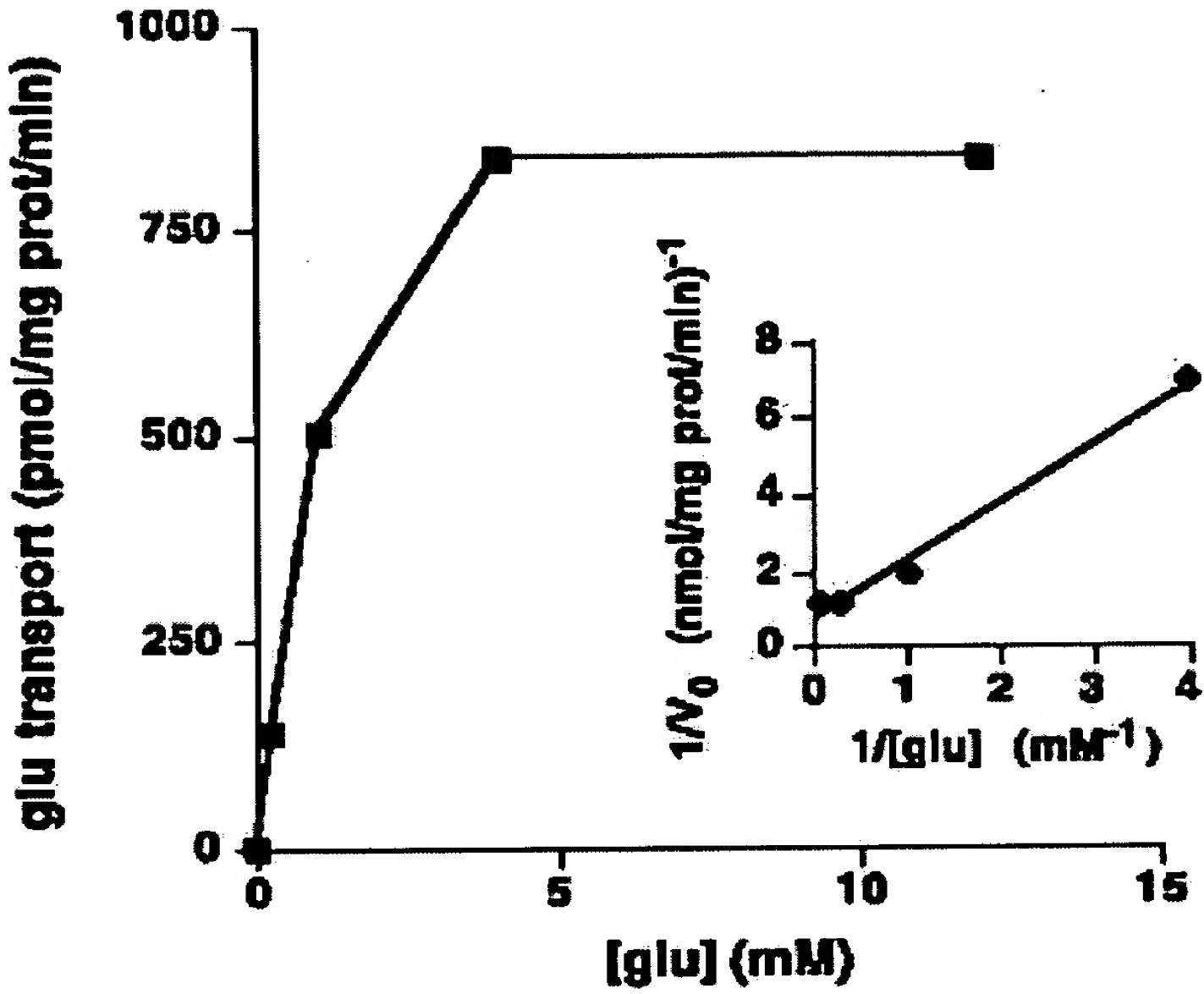


Fig. 2B

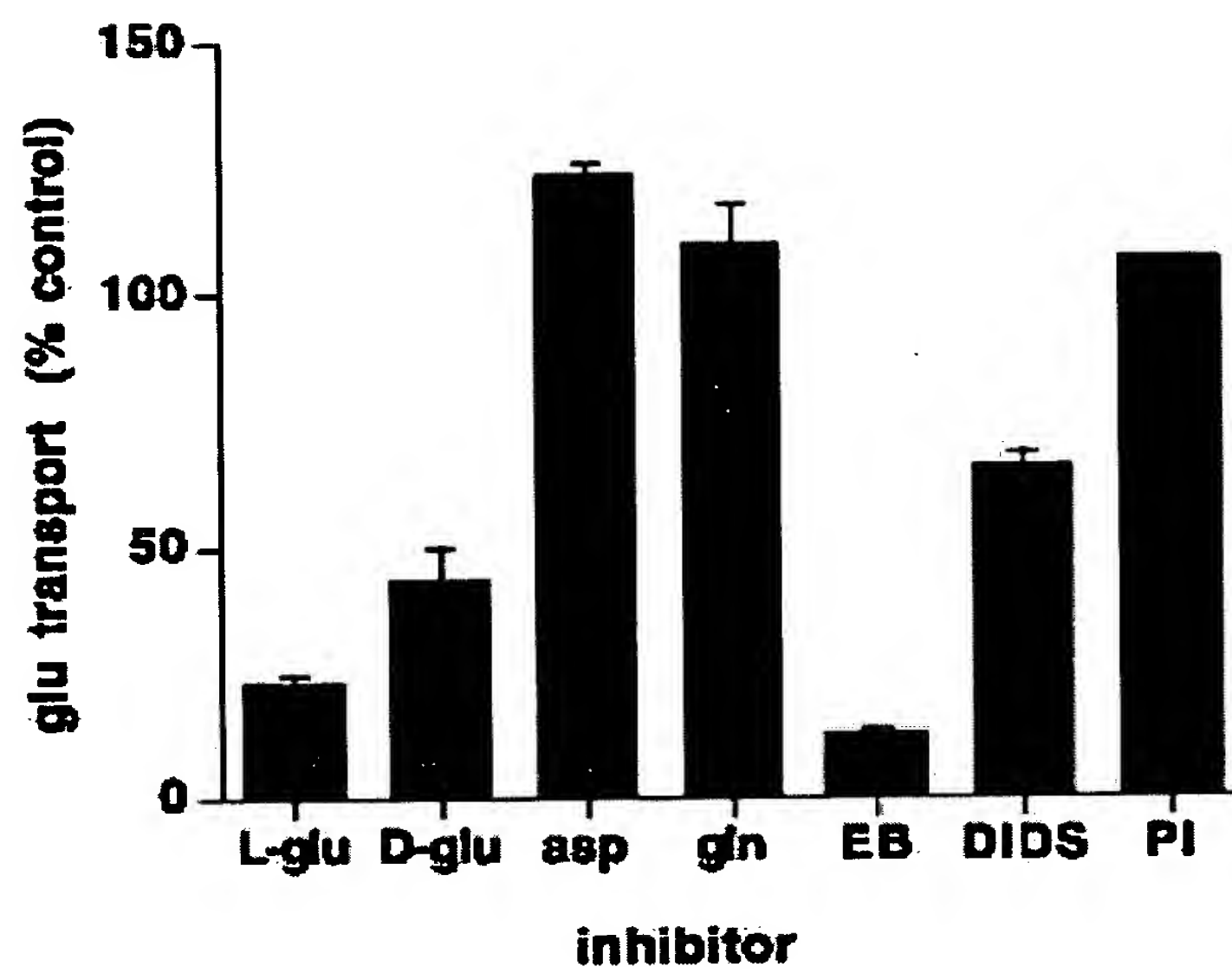


Fig. 3

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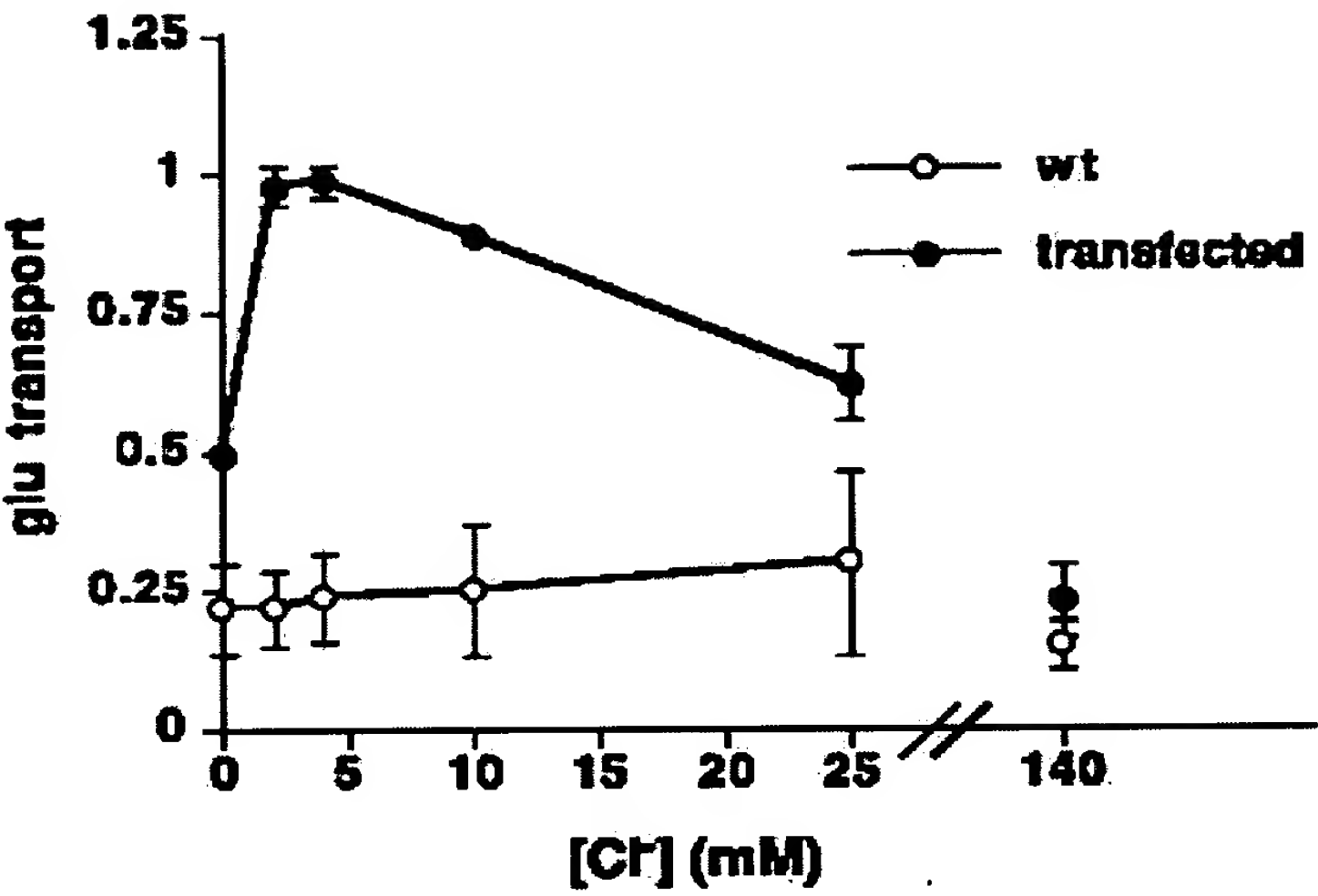


Fig. 4A

10420070750

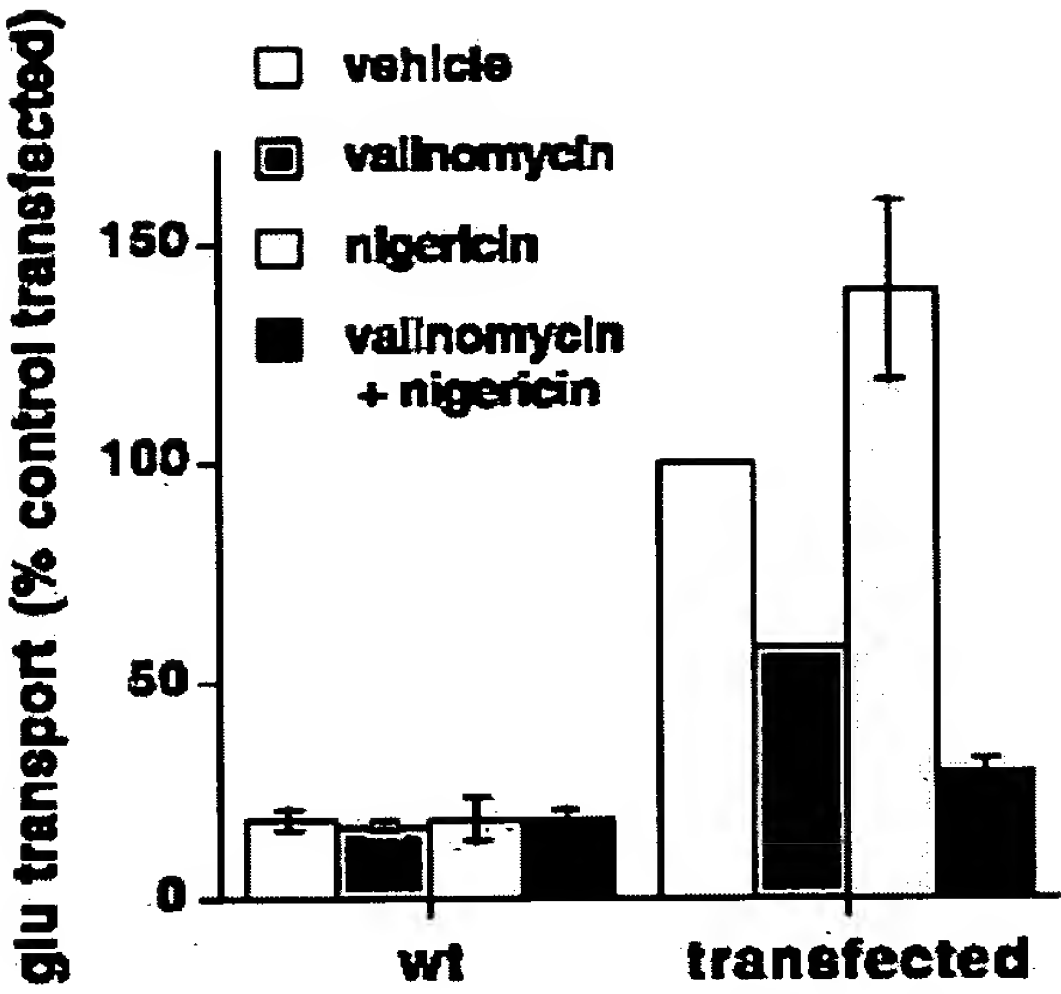


Fig. 4B

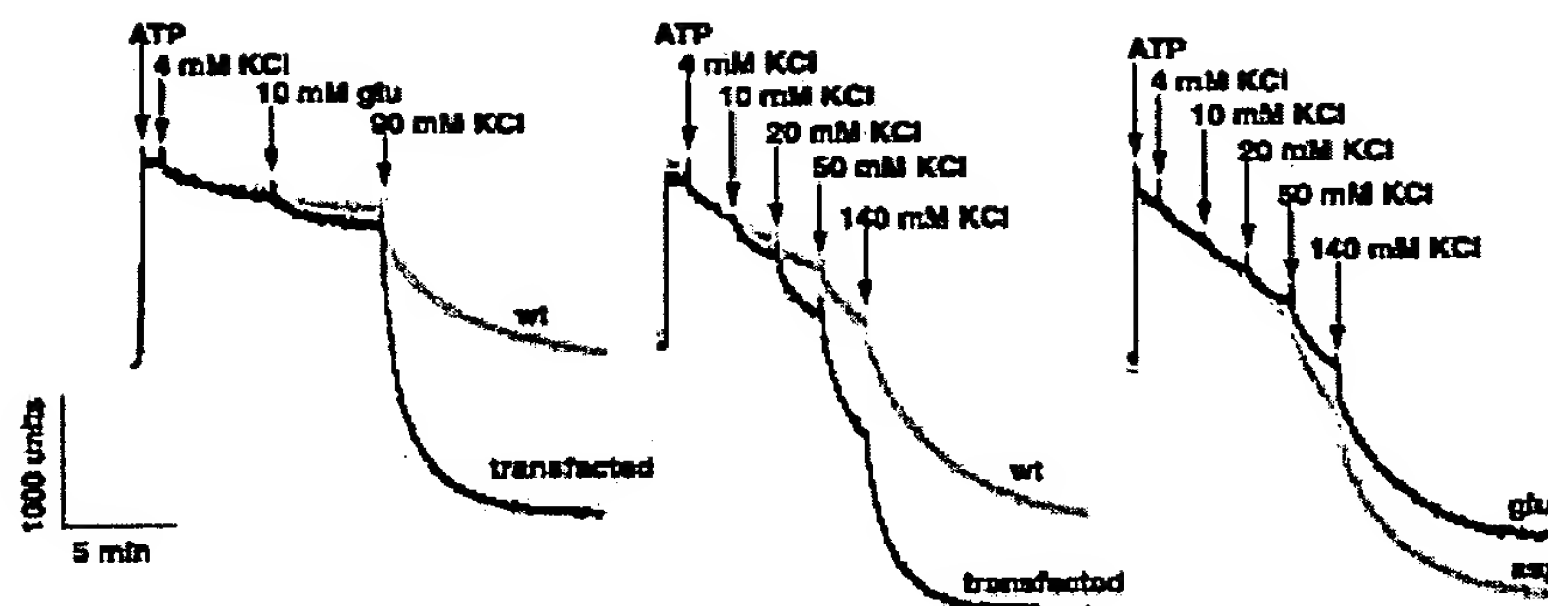


Fig. 5A

Fig. 5B

Fig. 5C

Fig. 5A, 5B, and 5C

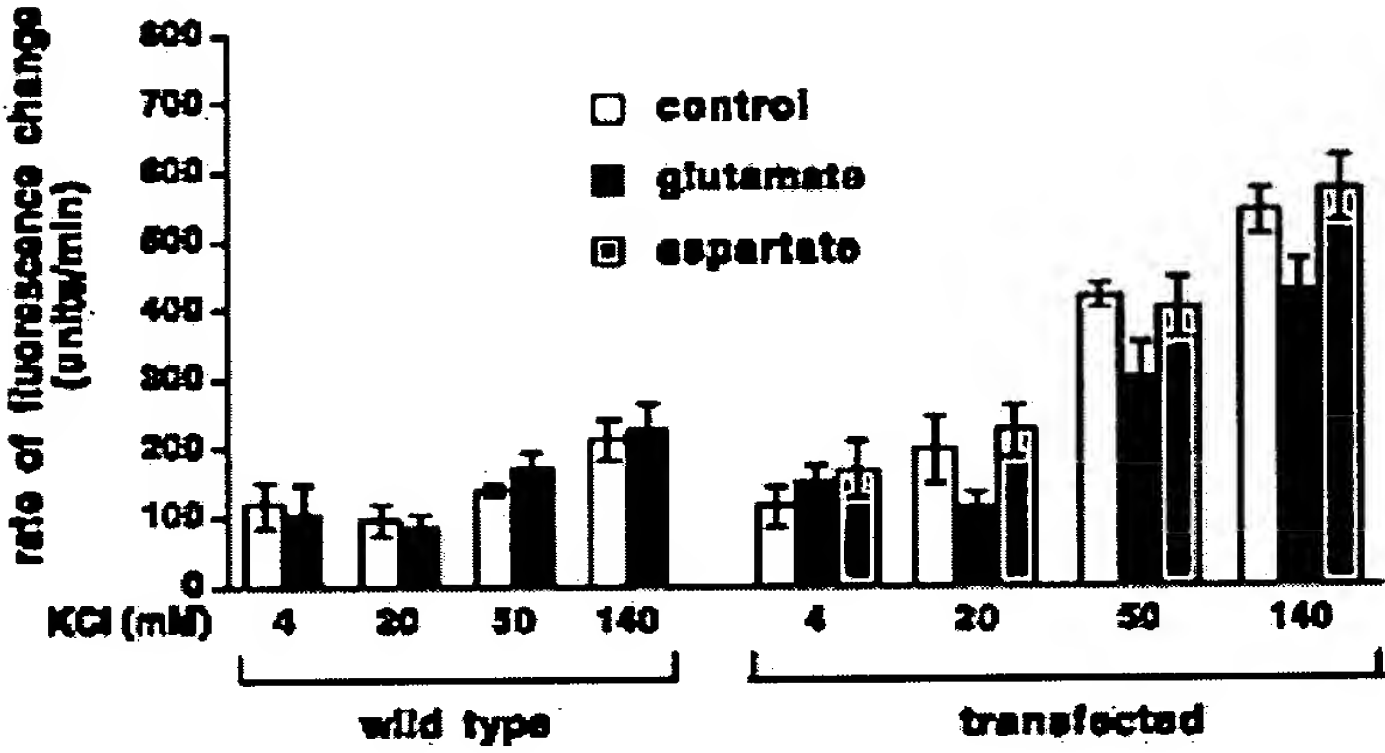


Fig. 5D

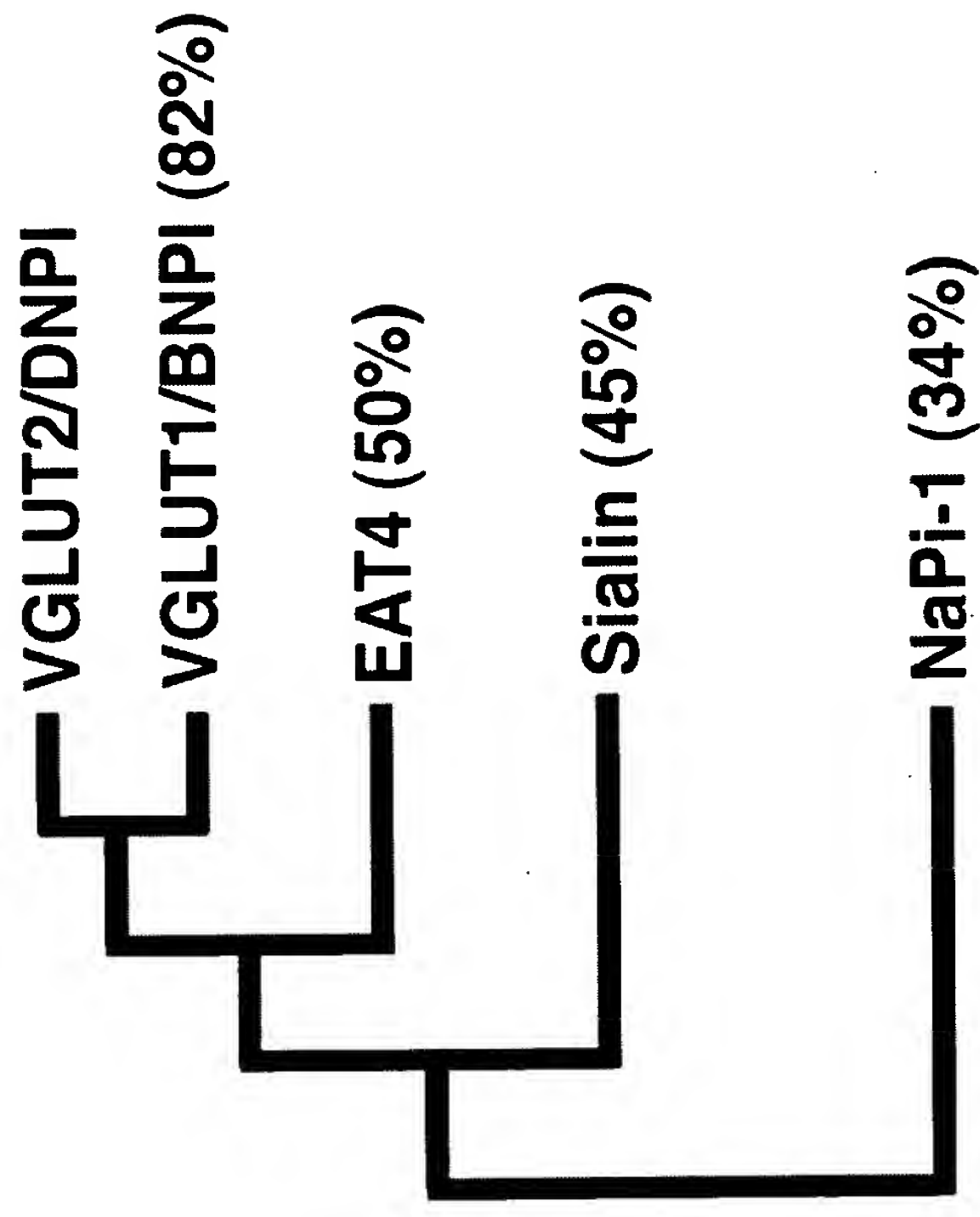


Fig. 6B

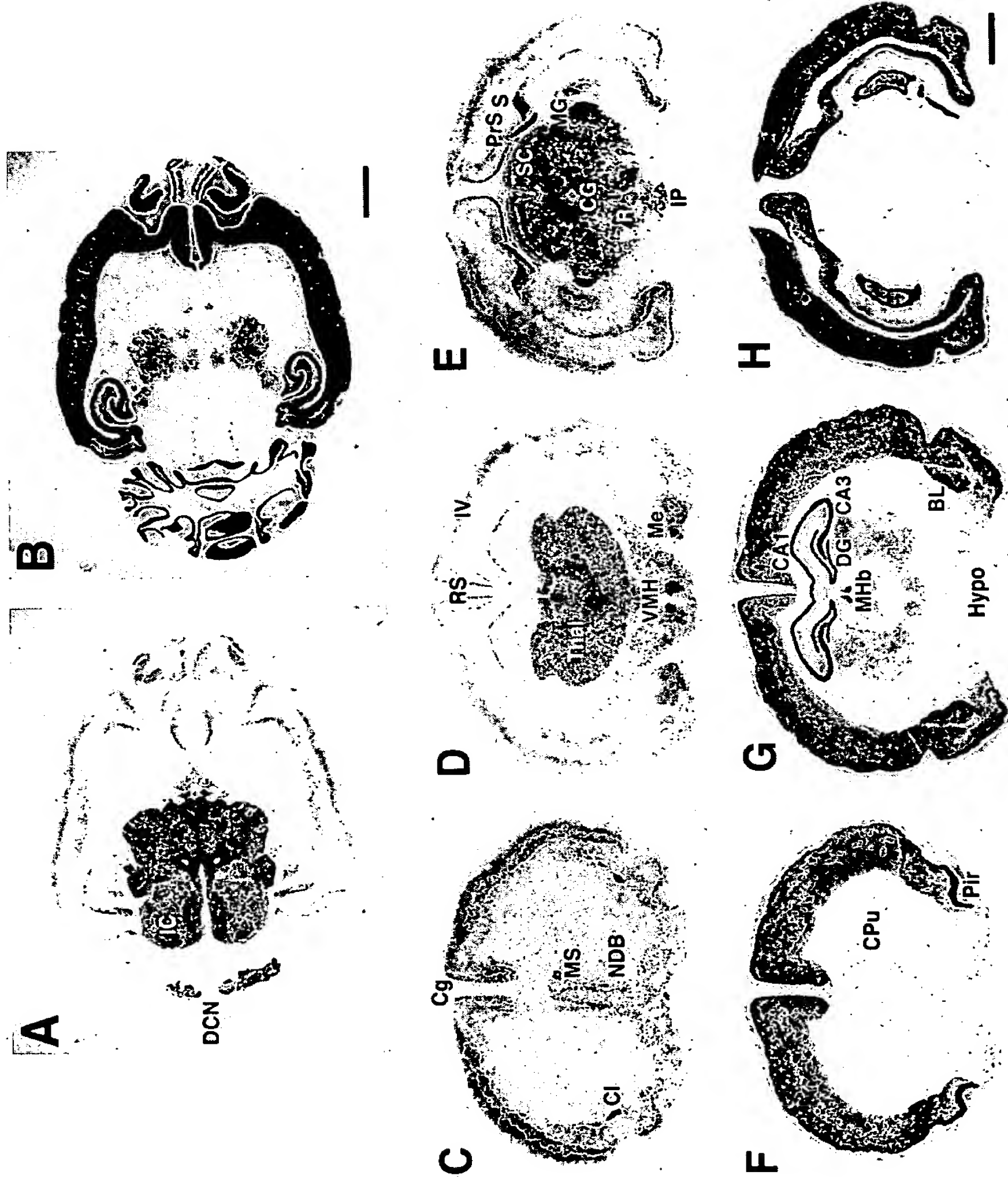


Fig. 7

VGLUT2

VGLUT1

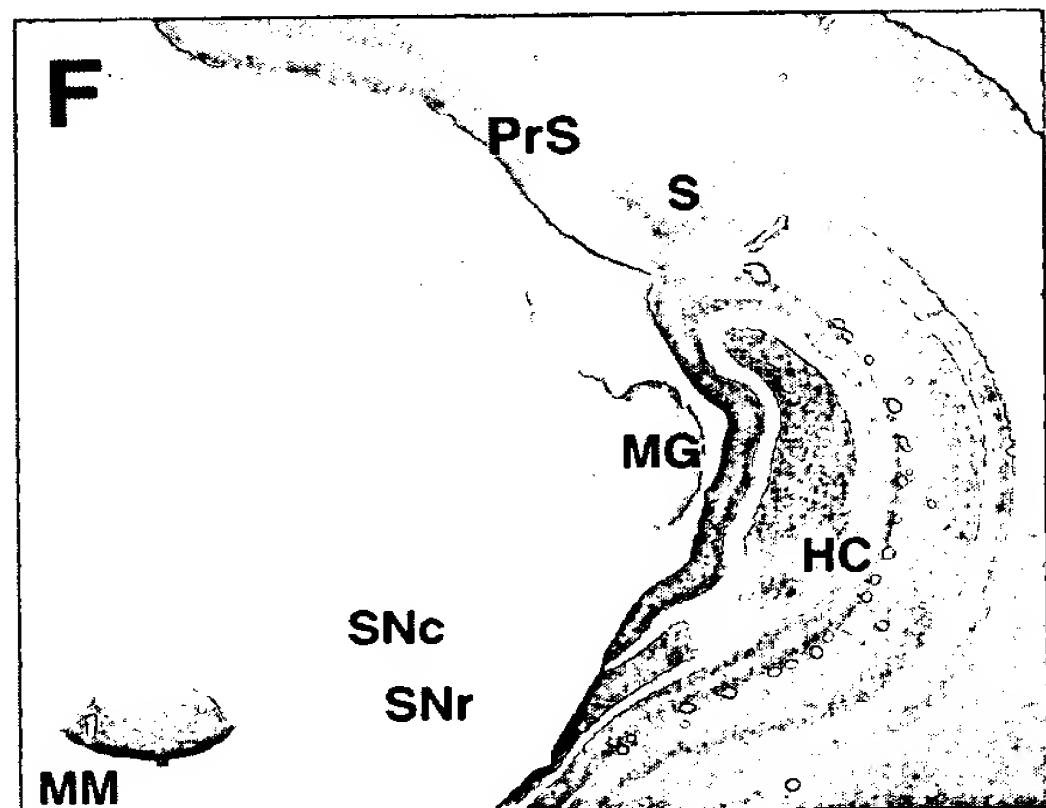
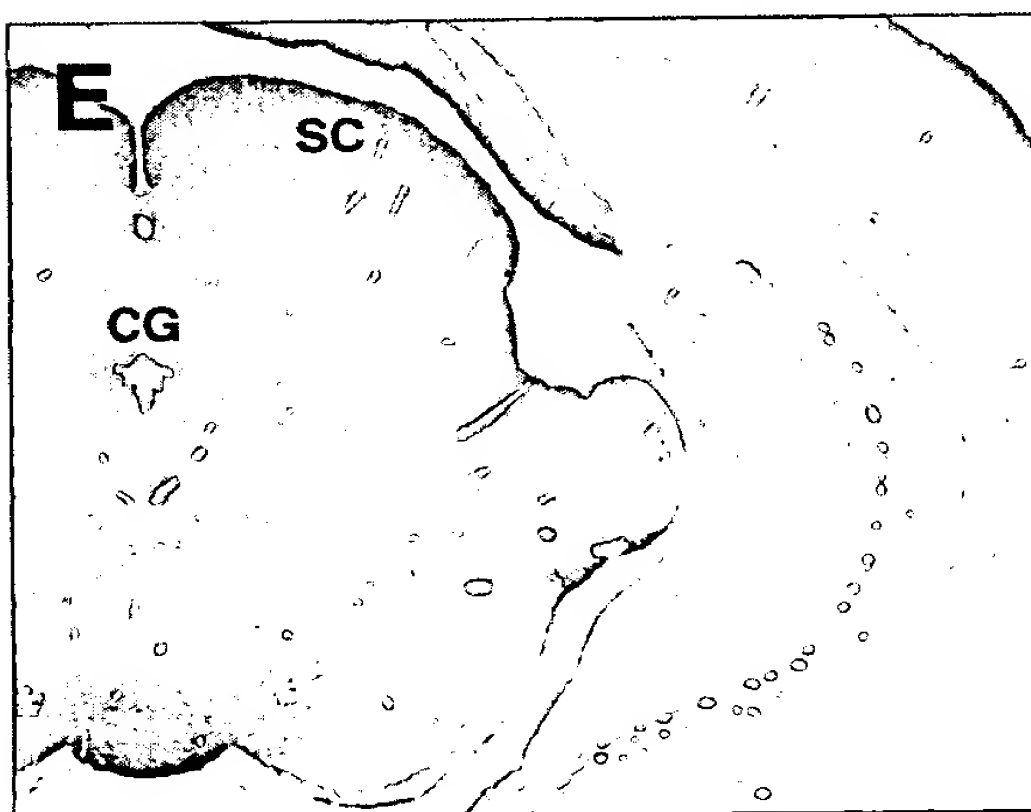
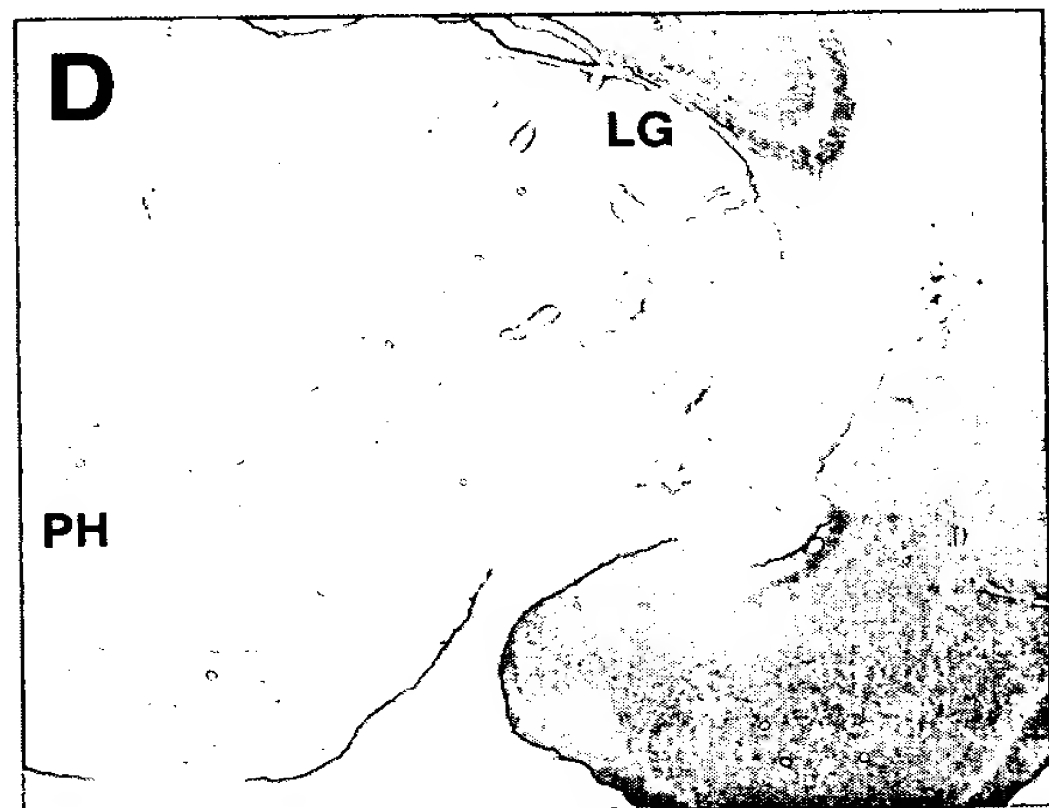
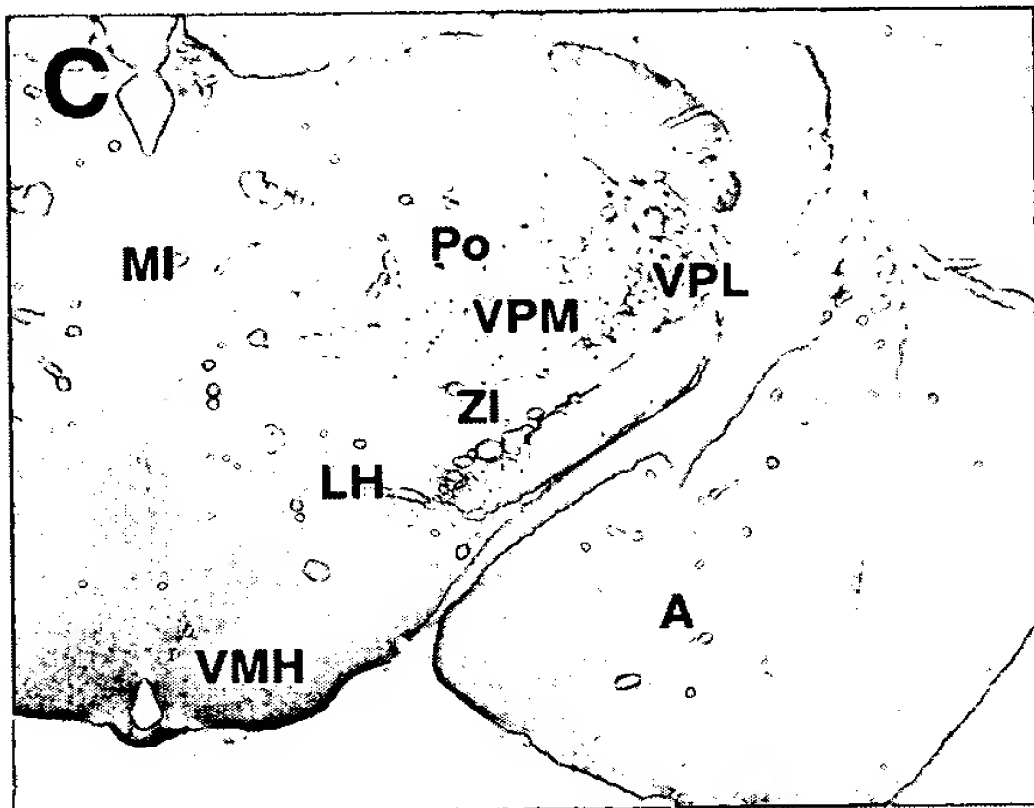
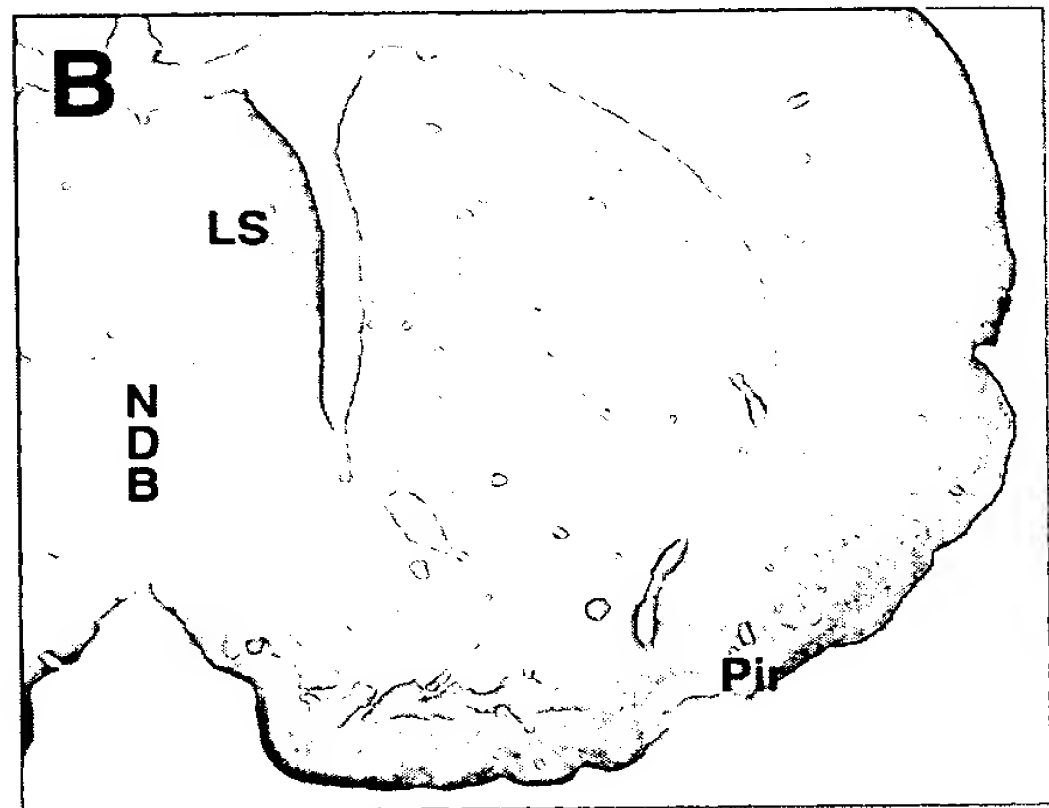
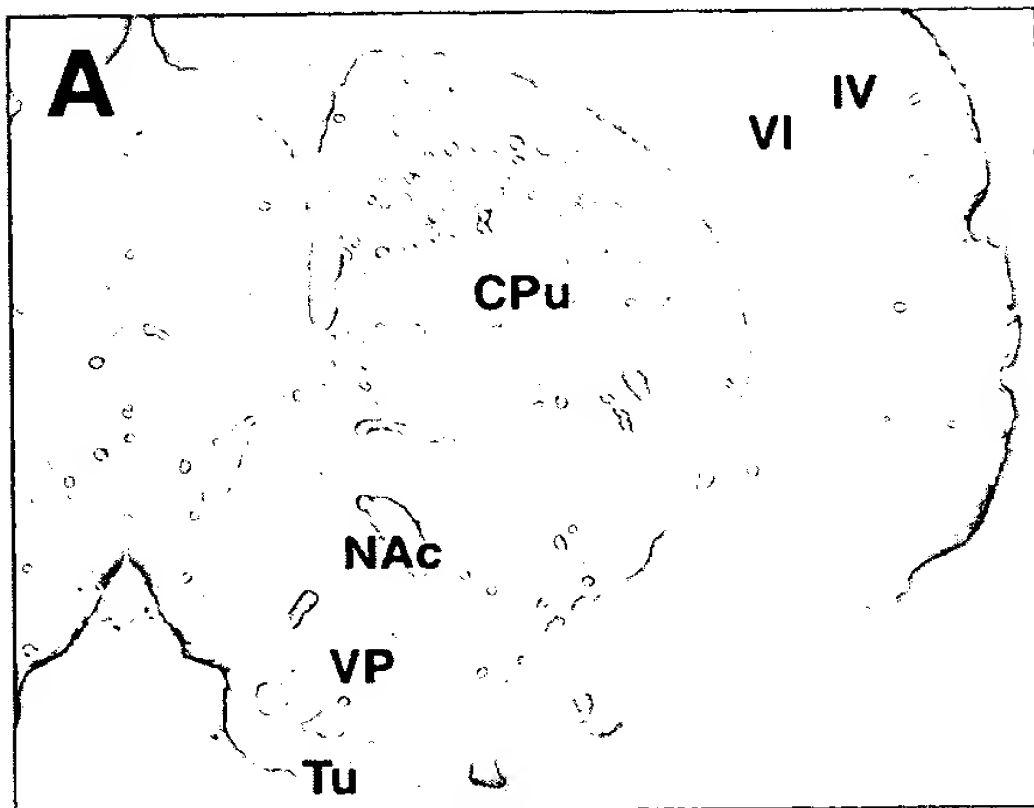


Fig. 8

0945434-070434

Fig. 9

Fig. 10A

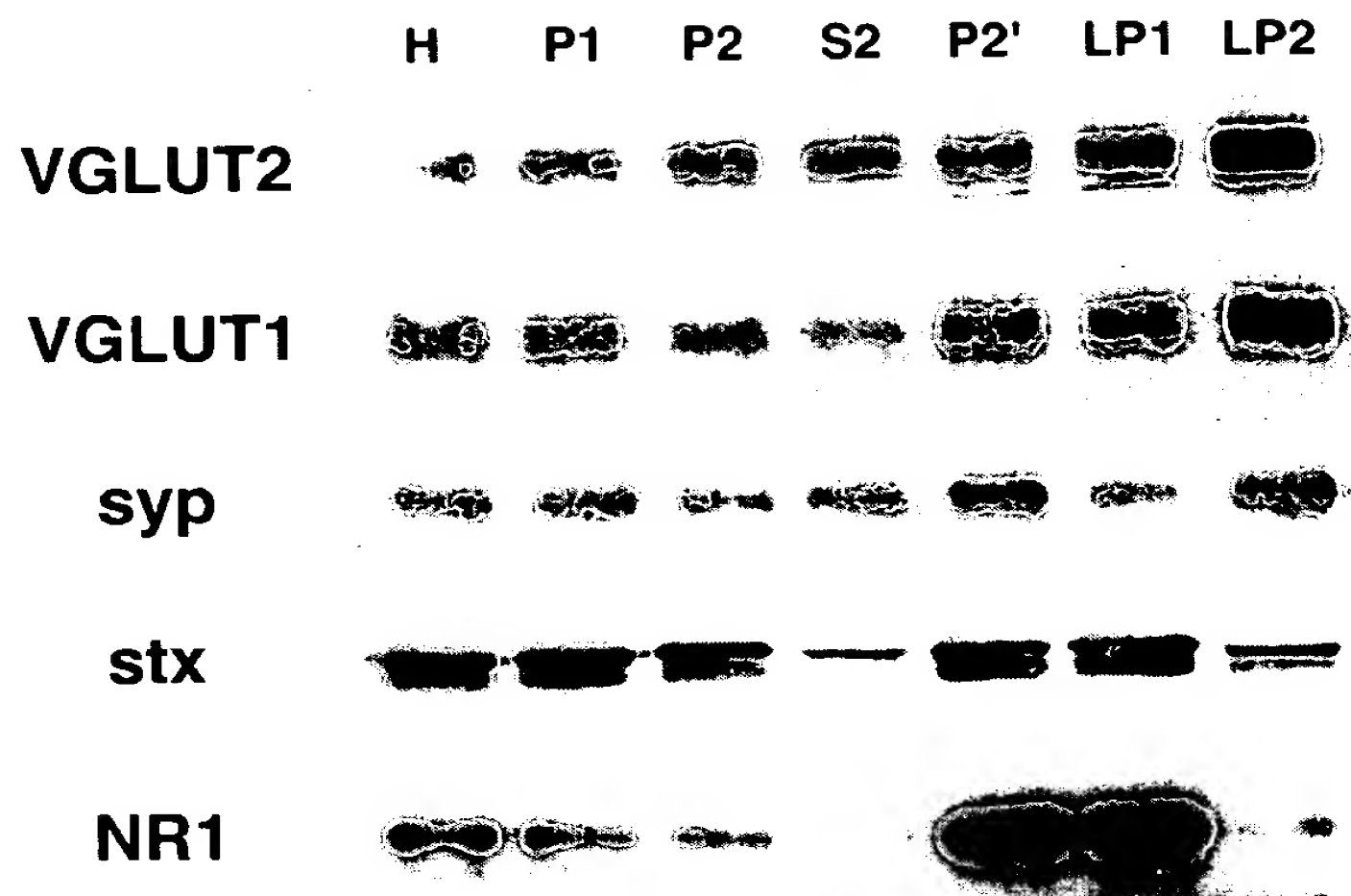
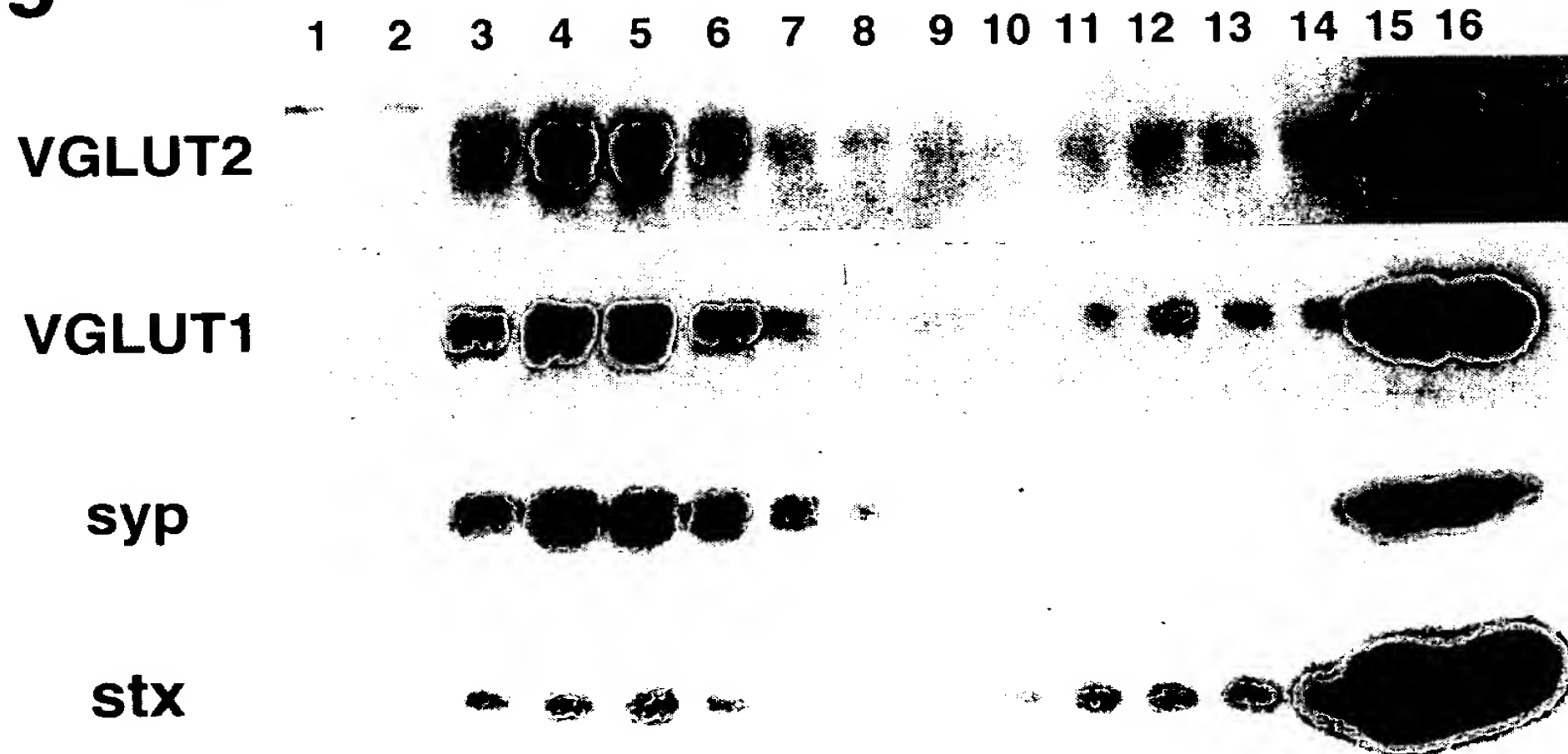


Fig. 10B



404220-13T5T50

Fig. 11A



Fig. 11B

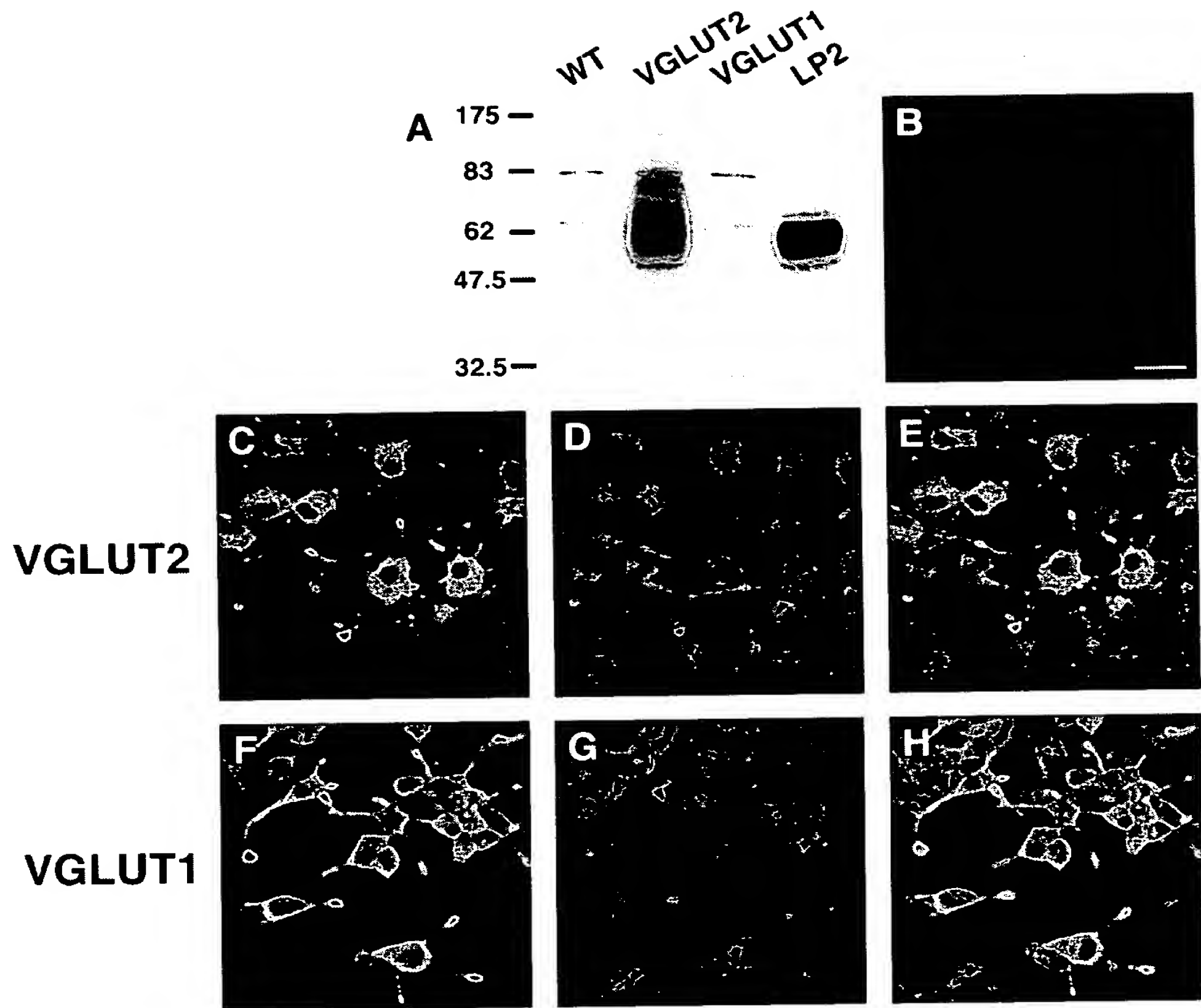


Fig. 12

Fig. 13A

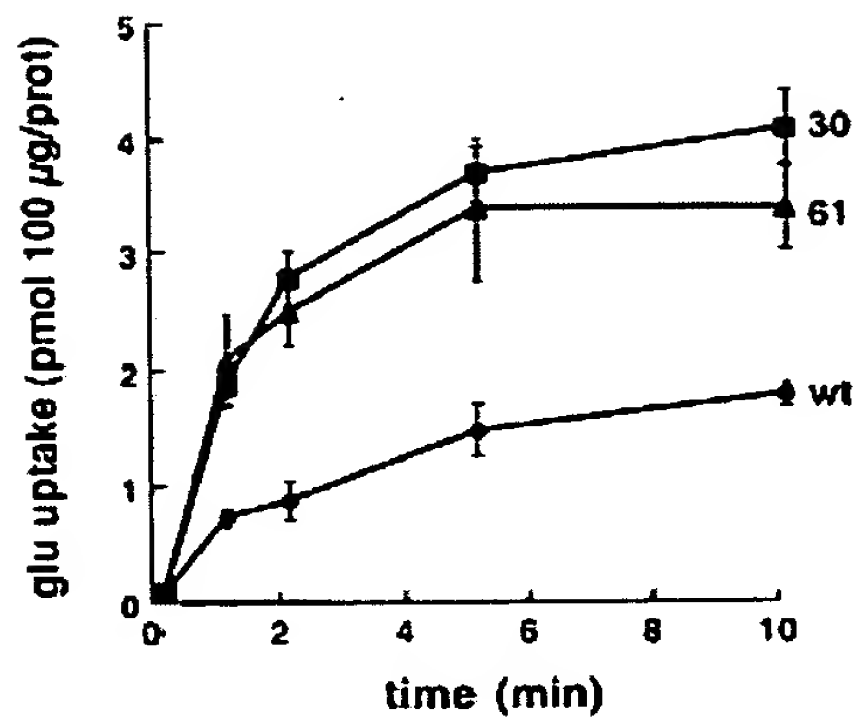


Fig. 13B

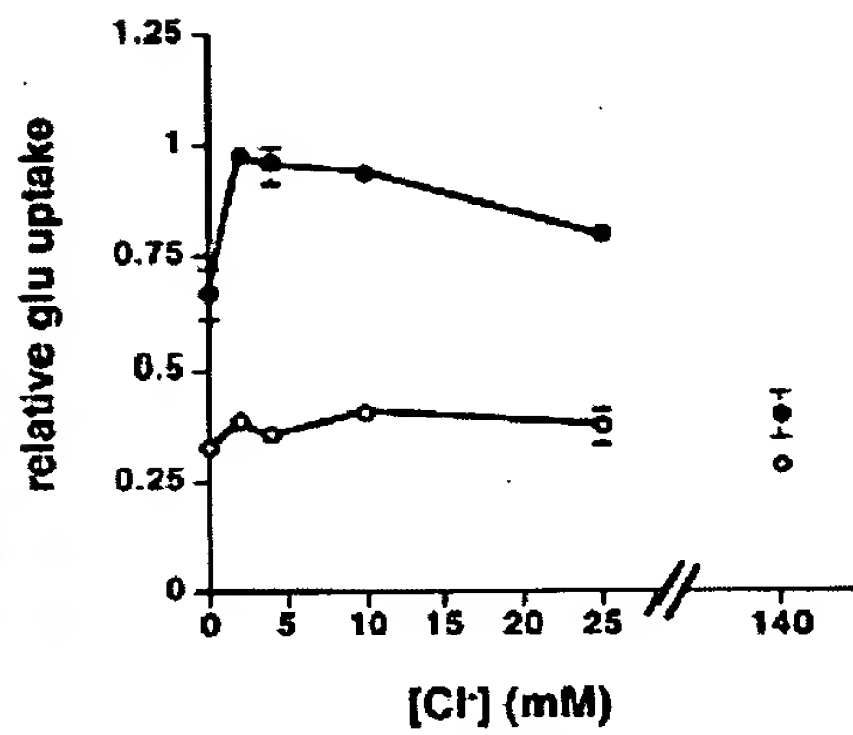
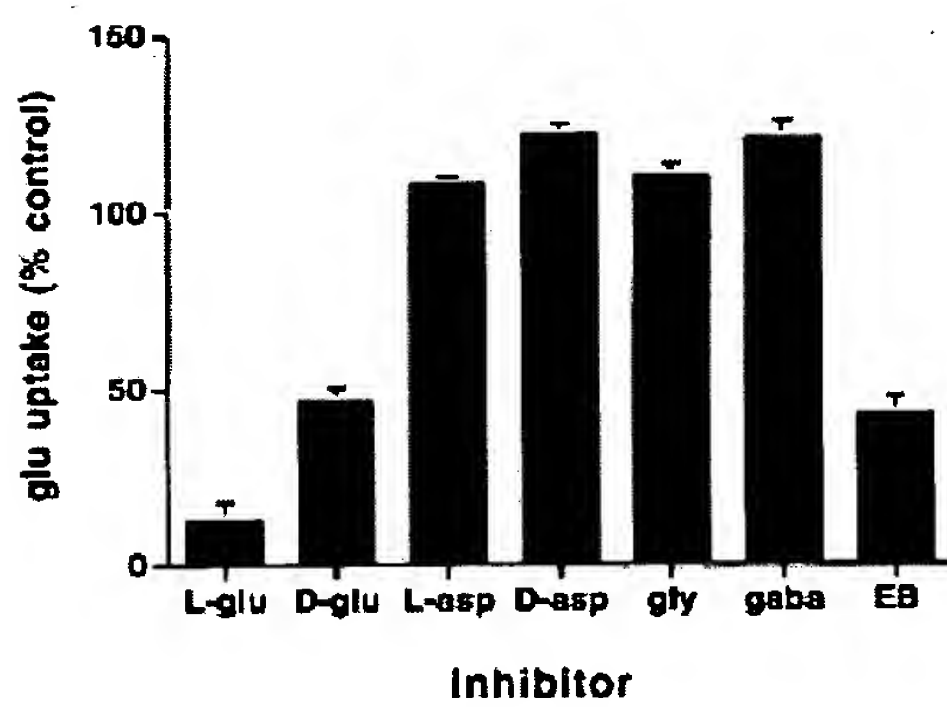
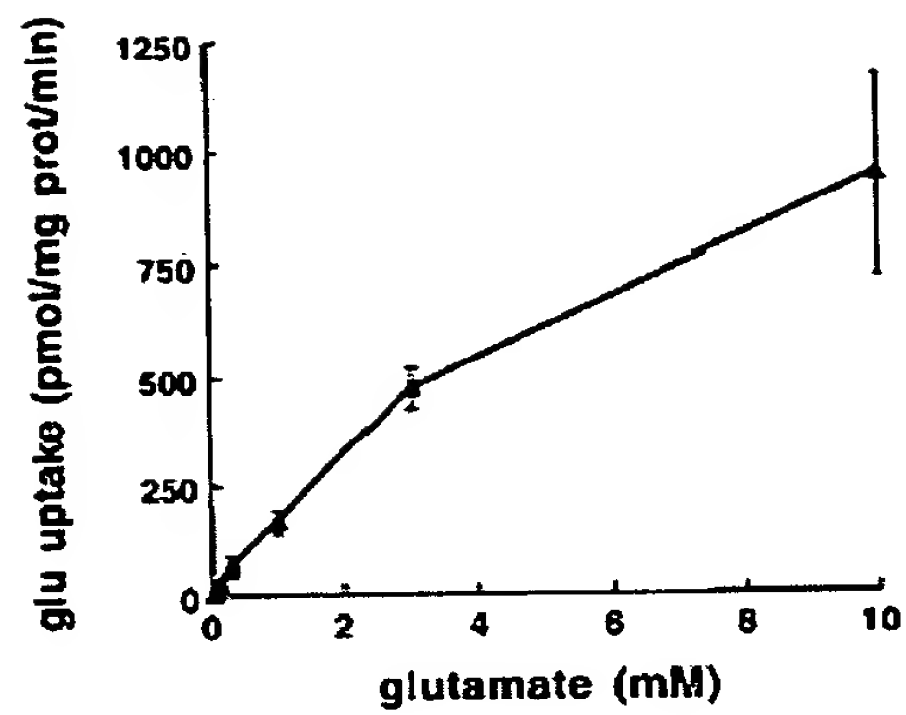


Fig. 13C

Fig. 13D

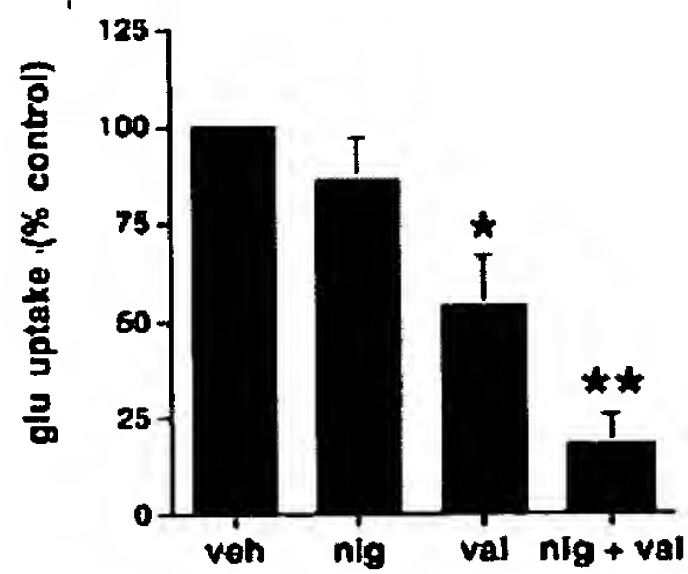


Fig. 13E